

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

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(i) APPLICANT: Papathanassiu, Adonia E  
Green, Shawn J.

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(ii) TITLE OF INVENTION: Compositions and Methods for  
Inhibiting Cellular Proliferation

(iii) NUMBER OF SEQUENCES: 2

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Jones & Askew  
(B) STREET: 191 Peachtree Street, 37th Floor  
(C) CITY: Atlanta  
(D) STATE: Georgia  
(E) COUNTRY: U.S.A.  
20 (F) ZIP: 30303

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

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(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(A) NAME: Greene, Jamie L.  
(B) REGISTRATION NUMBER: 32,467  
(C) REFERENCE/DOCKET NUMBER: 05213-0290

(ix) TELECOMMUNICATION INFORMATION:

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(A) TELEPHONE: (404) 818-3700  
(B) TELEFAX: (404) 818-3799

(2) INFORMATION FOR SEQ ID NO:1:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 276 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

25 (ix) FEATURE:  
(A) NAME/KEY: Active-site  
(B) LOCATION: 2..3  
(D) OTHER INFORMATION: /note= "Site of partial phosphorylation"

30 (ix) FEATURE:  
(A) NAME/KEY: Active-site  
(B) LOCATION: 117..118  
(D) OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"

35 (ix) FEATURE:  
(A) NAME/KEY: Active-site  
(B) LOCATION: 167..168  
(D) OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"

40 (ix) FEATURE:  
(A) NAME/KEY: Active-site  
(B) LOCATION: 228..229  
(D) OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"

45 (ix) FEATURE:  
(A) NAME/KEY: Domain  
(B) LOCATION: 26..76  
(D) OTHER INFORMATION: /label= Kunitz-1

## (ix) FEATURE:

5 (A) NAME/KEY: Domain  
 (B) LOCATION: 97..147  
 (D) OTHER INFORMATION: /label= Kunitz-2

## (ix) FEATURE:

10 (A) NAME/KEY: Domain  
 (B) LOCATION: 189..239  
 (D) OTHER INFORMATION: /label= Kunitz-3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu  
 1 5 10 15

Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp  
 20 25 30

20 Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr  
 35 40 45

Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn  
 25 50 55 60

Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn  
 65 70 75 80

30 Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe  
 85 90 95

Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg  
 100 105 110

35 Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly  
 115 120 125

Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys  
 40 130 135 140

Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly  
 145 150 155 160

45 Thr Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys  
 165 170 175

Val Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro  
 180 185

Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn  
195 200 205

5 Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly  
210 215 220

Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys  
10 225 230 235 240

Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys  
245 250 255

15 Arg Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe  
260 265 270

Val Lys Asn Met  
275

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25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 213 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5	Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu	1	5	10	15
	Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr	20	25	30	
10	Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu	35	40	45	
	Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp Asp Ala Cys	50	55	60	
15	Trp Arg Ile Glu Lys Val Pro Lys Val Cys Arg Leu Gln Val Ser Val	65	70	75	80
	Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys Tyr Phe Phe Asn Leu Ser	85	90	95	
20	Ser Met Thr Cys Glu Lys Phe Phe Ser Gly Gly Cys His Arg Asn Arg	100	105	110	
	Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr Cys Met Gly Phe Cys Ala	115	120	125	
25	Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu	130	135	140	
	Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr	145	150	155	160
30	Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn Asn Phe	165	170	175	
	Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys	180	185	190	
35	Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile	195	200	205	
	Arg Lys Lys Gln Phe	210			
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